

1646

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/521,195

DATE: 08/07/2001

TIME: 13:22:26

Input Set : A:\06501-057001.txt

Output Set: N:\CRF3\08072001\I521195.raw

3 <110> APPLICANT: Nezu, Jun-Ichi
 4 Oku, Asuka
 6 <120> TITLE OF INVENTION: TRANSPORTER GENES
 8 <130> FILE REFERENCE: 06501-057001
 10 <140> CURRENT APPLICATION NUMBER: 09/521,195
 11 <141> CURRENT FILING DATE: 2000-03-07
 13 <150> PRIOR APPLICATION NUMBER: JP 10/156660
 14 <151> PRIOR FILING DATE: 1998-05-20
 16 <150> PRIOR APPLICATION NUMBER: JP 9/260972
 17 <151> PRIOR FILING DATE: 1997-09-08
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04009
 20 <151> PRIOR FILING DATE: 1998-09-07
 22 <160> NUMBER OF SEQ ID NOS: 32
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 551
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
 30 Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro
 31 1 5 10 15
 32 Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
 33 20 25 30
 34 Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
 35 35 40 45
 36 Arg Cys Arg Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn
 37 50 55 60
 38 Asn Ser Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His Ser
 39 65 70 75 80
 40 Cys Ser Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly
 41 85 90 95
 42 Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser
 43 100 105 110
 44 Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Val
 45 115 120 125
 46 Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asn Trp Lys Val Pro Leu
 47 130 135 140
 48 Thr Thr Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Val Ser
 49 145 150 155 160
 50 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Ala Thr
 51 165 170 175
 52 Met Ala Val Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Ile Ser
 53 180 185 190
 54 Trp Glu Met Phe Thr Val Leu Phe Val Ile Val Gly Met Gly Gln Ile
 55 195 200 205
 56 Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Gly Lys
 57 210 215 220
 58 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala

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59 225                230                235                240
60 Val Gly Tyr Met Leu Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
61                245                250                255
62 Arg Met Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Val Pro
63                260                265                270
64 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
65                275                280                285
66 Arg Phe Arg Glu Ala Glu Asp Ile Ile Gln Lys Ala Ala Lys Met Asn
67                290                295                300
68 Asn Thr Ala Val Pro Ala Val Ile Phe Asp Ser Val Glu Glu Leu Asn
69 305                310                315                320
70 Pro Leu Lys Gln Gln Lys Ala Phe Ile Leu Asp Leu Phe Arg Thr Arg
71                325                330                335
72 Asn Ile Ala Ile Met Thr Ile Met Ser Leu Leu Leu Trp Met Leu Thr
73                340                345                350
74 Ser Val Gly Tyr Phe Ala Leu Ser Leu Asp Ala Pro Asn Leu His Gly
75                355                360                365
76 Asp Ala Tyr Leu Asn Cys Phe Leu Ser Ala Leu Ile Glu Ile Pro Ala
77                370                375                380
78 Tyr Ile Thr Ala Trp Leu Leu Arg Thr Leu Pro Arg Arg Tyr Ile
79 385                390                395                400
80 Ile Ala Ala Val Leu Phe Trp Gly Gly Gly Val Leu Leu Phe Ile Gln
81                405                410                415
82 Leu Val Pro Val Asp Tyr Tyr Phe Leu Ser Ile Gly Leu Val Met Leu
83                420                425                430
84 Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val Phe Thr
85                435                440                445
86 Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly Val Thr
87                450                455                460
88 Ser Thr Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe Val Tyr
89 465                470                475                480
90 Leu Gly Ala Tyr Asn Arg Met Leu Pro Tyr Ile Val Met Gly Ser Leu
91                485                490                495
92 Thr Val Leu Ile Gly Ile Phe Thr Leu Phe Phe Pro Glu Ser Leu Gly
93                500                505                510
94 Met Thr Leu Pro Glu Thr Leu Glu Gln Met Gln Lys Val Lys Trp Phe
95                515                520                525
96 Arg Ser Gly Lys Lys Thr Arg Asp Ser Met Glu Thr Glu Glu Asn Pro
97                530                535                540
98 Lys Val Leu Ile Thr Ala Phe
99 545                550
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 2135
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <220> FEATURE:
107 <221> NAME/KEY: CDS
108 <222> LOCATION: (147)..(1799)
110 <400> SEQUENCE: 2

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111 ccccggttc gcgcccgaat ttctaacagc ctgcctgtcc cccgggaacg ttctaacatc      60
113 cttggggagc gccccagcta caagacactg tcctgagaac gctgtcatca cccgtagttg      120
115 caagtttcgg agcggcagtg ggaagc atg cgg gac tac gac gag gtg atc gcc      173
116                               Met Arg Asp Tyr Asp Glu Val Ile Ala
117                               1                               5
119 ttc ctg ggc gag tgg ggg ccc ttc cag cgc ctc atc ttc ttc ctg ctc      221
120 Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
121 10                               15                               20                               25
123 agc gcc agc atc atc ccc aat ggc ttc aat ggt atg tca gtc gtg ttc      269
124 Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
125                               30                               35                               40
127 ctg gcg ggg acc ccg gag cac cgc tgt cga gtg ccg gac gcc gcg aac      317
128 Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
129                               45                               50                               55
131 ctg agc agc gcc tgg cgc aac aac agt gtc ccg ctg cgg ctg cgg gac      365
132 Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
133                               60                               65                               70
135 ggc cgc gag gtg ccc cac agc tgc agc cgc tac cgg ctc gcc acc atc      413
136 Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
137                               75                               80                               85
139 gcc aac ttc tcg gcg ctc ggg ctg gag ccg ggg cgc gac gtg gac ctg      461
140 Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu
141 90                               95                               100                               105
143 ggg cag ctg gag cag gag agc tgc ctg gat ggc tgg gag ttc agc cag      509
144 Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
145                               110                               115                               120
147 gac gtc tac ctg tcc acc gtc gtg acc gag tgg aat ctg gtg tgt gag      557
148 Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
149                               125                               130                               135
151 gac aac tgg aag gtg ccc ctc acc acc tcc ctg ttc ttc gta ggc gtg      605
152 Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
153                               140                               145                               150
155 ctc ctc ggc tcc ttc gtg tcc ggg cag ctg tca gac agg ttt ggc agg      653
156 Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
157                               155                               160                               165
159 aag aac gtt ctc ttc gca acc atg gct gta cag act ggc ttc agc ttc      701
160 Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
161 170                               175                               180                               185
163 ctg cag att ttc tcc atc agc tgg gag atg ttc act gtg tta ttt gtc      749
164 Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
165                               190                               195                               200
167 atc gtg ggc atg ggc cag atc tcc aac tat gtg gta gcc ttc ata cta      797
168 Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
169                               205                               210                               215
171 gga aca gaa att ctt ggc aag tca gtt cgt att ata ttc tct aca tta      845
172 Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
173                               220                               225                               230
175 gga gtg tgc aca ttt ttt gca gtt ggc tat atg ctg ctg cca ctg ttt      893
176 Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe

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177	235	240	245	
179	gct tac ttc atc aga gac tgg cgg atg ctg ctg ctg gcg ctg acg gtg			941
180	Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val			
181	250	255	260	265
183	ccg gga gtg ctg tgt gtc ccg ctg tgg tgg ttc att cct gaa tct ccc			989
184	Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro			
185	270	275	280	
187	cga tgg ctg ata tcc cag aga aga ttt aga gag gct gaa gat atc atc			1037
188	Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile			
189	285	290	295	
191	caa aaa gct gca aaa atg aac aac aca gct gta cca gca gtg ata ttt			1085
192	Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe			
193	300	305	310	
195	gat tct gtg gag gag cta aat ccc ctg aag cag cag aaa gct ttc att			1133
196	Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile			
197	315	320	325	
199	ctg gac ctg ttc agg act cgg aat att gcc ata atg acc att atg tct			1181
200	Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser			
201	330	335	340	345
203	ttg ctg cta tgg atg ctg acc tca gtg ggt tac ttt gct ctg tct ctg			1229
204	Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu			
205	350	355	360	
207	gat gct cct aat tta cat gga gat gcc tac ctg aac tgt ttc ctc tct			1277
208	Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser			
209	365	370	375	
211	gcc ttg att gaa att cca gct tac att aca gcc tgg ctg cta ttg cga			1325
212	Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Leu Arg			
213	380	385	390	
215	acg ctg ccc agg cgt tat atc ata gct gca gta ctg ttc tgg gga gga			1373
216	Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly			
217	395	400	405	
219	ggt gtg ctt ctc ttc att caa ctg gta cct gtg gat tat tac ttc tta			1421
220	Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu			
221	410	415	420	425
223	tcc att ggt ctg gtc atg ctg gga aaa ttt ggg atc acc tct gct ttc			1469
224	Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe			
225	430	435	440	
227	tcc atg ctg tat gtc ttc act gct gag ctc tac cca acc ctg gtc agg			1517
228	Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg			
229	445	450	455	
231	aac atg gcg gtg ggg gtc aca tcc acg gcc tcc aga gtg ggc agc atc			1565
232	Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile			
233	460	465	470	
235	att gcc ccc tac ttt gtt tac ctc ggt gct tac aac aga atg ctg ccc			1613
236	Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro			
237	475	480	485	
239	tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt			1661
240	Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu			
241	490	495	500	505

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243 ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag      1709
244 Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
245          510          515          520
247 atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aca aga gac tca      1757
248 Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
249          525          530          535
251 atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc      1799
252 Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
253          540          545          550
255 tgaaaaaata tctaccccat ttggtgaagt gaaaaacaga aaaataagac cctgtggaga      1859
257 aattcgttgt tcccactgaa atggactgac tgtaacgatt gacacaaaa tgaaccttgc      1919
259 tatcaagaaa tgctcgtcat acagtaaact ctggatgatt cttccagata atgtccttgc      1979
261 tttaaaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg      2039
263 taagatgtct tgaaaacatg ttagtcaagg actggtaaaa tacatataaa gattaacact      2099
265 catttccaat catacaaata ctatccaaat aaaaaa      2135
267 <210> SEQ ID NO: 3
268 <211> LENGTH: 557
269 <212> TYPE: PRT
270 <213> ORGANISM: Homo sapiens
272 <400> SEQUENCE: 3
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276 Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro
277 20 25 30
279 Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu
280 35 40 45
282 His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
283 50 55 60
285 Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His
286 65 70 75
288 Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
289 80 85 90 95
291 Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
292 100 105 110
294 Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
295 115 120 125
297 Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
298 130 135 140
300 Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
301 145 150 155
303 Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
304 160 165 170 175
306 Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
307 180 185 190
309 Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
310 195 200 205
312 Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
313 210 215 220
315 Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr

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VERIFICATION SUMMARY

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Input Set : A:\06501-057001.txt

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